

REMARKS

Formal Matters

Claims 20, 22, 26-28 and 31-36 remain in this application. Claims 20, 26 and 33-36 are amended. The Examiner has acknowledged that Claim 31 is directed to allowable subject matter. No new matter is added by the amendments.

Support for the amendments is found throughout the specification, such as at page 2, lines 36-37.

In view of the Examiner's earlier restriction requirement, applicant retains the right to present withdrawn and cancelled subject matter in continuing prosecution (*e.g.*, continuations and divisionals).

Applicants acknowledge the informal nature of the drawings and respectfully request that the Examiner hold the objection in abeyance until agreement can be reached for allowable subject matter.

Applicants further acknowledge the Examiner's comment with respect to inclusion of the sequence listing in the Figures. However, both 37 C.F.R. § 1.58(a) and 37 C.F.R. § 1.83 indicate an exception to these requirements for applications filed under 35 U.S.C. § 371 (U.S. National phase of PCT filing). The present application was filed under 35 U.S.C. § 371.

Rejection Under 35 U.S.C. § 112, Second Paragraph

Claim 20 is rejected under 35 U.S.C. § 112, second paragraph allegedly as being indefinite for failing to particularly point out and distinctly claim the subject matter of the invention.

In response, Applicants amendment renders the rejection moot.

Rejection Under 35 U.S.C. § 102(e)

Claims 20, 22, 26-28 and 32-36 are rejected under 35 U.S.C. § 102(e) allegedly as being anticipated by Sims *et al.*, US2003/0091532. Specifically, the Examiner alleges that Sims *et al.*,

describes an amino acid sequence of 192 residues as SEQ ID NO:3 that comprises residues 22-203 of SEQ ID NO:5 in the present application.

In response, Applicants respectfully note that the filing date of the cited US2003/0091532 application is 15 May 2003. Thus, the effective date of US2003/0096339 for prior art purposes under 35 U.S.C. § 102(e) is 15 May 2003. Applicants respectfully also note the corresponding International PCT application, WO 00/36108, published on 22 June 2000. Thus, the effective date of WO 00/36108 for prior art purposes is 22 June 2000.

Applicants had intended to enclose herewith a declaration under 37 U.S.C. § 1.131 signed by Audrey Goddard, Ph.D. (an inventor of the claimed invention) which effectively swears behind the US2003/0091532 (and WO 00/91532) reference, thereby effectively removing this references as a publication that can be relied upon in support of a rejection under 35 U.S.C. § 102(e). However, due to her travel schedule, Dr. Goddard was unavailable to execute this Declaration. In this Declaration, Dr. Goddard will provide facts demonstrating that the Applicants have reduced to practice the claimed IL1-1Ra1 polypeptide sequences prior to 22 June 2000. Applicants will convey this Declaration when Dr. Goddard becomes available again, and respectfully request consideration of this Declaration at such time.

Applicants respectfully request reconsideration and withdrawal of the rejection of Claims 20, 22, 26-28 and 32-36 under 35 U.S.C. § 102(e) as being anticipated by Sims *et al.* US2003/0091532.

SUMMARY

Claims 20, 22, 26-28 and 31-40 are pending in the application.

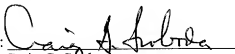
If in the opinion of the Examiner, a **telephone conference** would expedite the prosecution of the subject application, the Examiner is **strongly encouraged** to call the undersigned at the number indicated below.

This response/amendment is submitted with a transmittal letter and petition for a Three-month extension of time and fees. In the unlikely event that this document is separated from the transmittal letter or if fees are required, applicants petition the Commissioner to authorize charging our Deposit Account 07-0630 for any fees required or credits due and any extensions of time necessary to maintain the pendency of this application.

Applicants respectfully request that a timely Notice of Allowance be issued in this case.

Respectfully submitted,
GENENTECH, INC.

Date: **July 11, 2006**

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199753

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Appendix

USSN 60/113,430

IL-1 RELATED POLYPEPTIDES

FIELD OF THE INVENTION

The present invention relates generally to the identification and isolation of novel DNAs having homology to interleukin-1 (IL-1) or interleukin-1 receptor antagonist (IL-1Ra) polypeptides, and to the recombinant production of novel polypeptides, designated herein as interleukin-1-like polypeptides ("IL-1p").

BACKGROUND OF THE INVENTION

Interleukin-1 refers to two proteins (IL-1 α and IL-1 β) which play a key role early in the inflammatory response (for a review, see Dinarello, *Blood*, 87: 2095-2147 (1996) and references therein). both proteins are made as intracellular precursor proteins which are cleaved upon secretion to yield mature carboxy-terminal 17 kDa fragments which are biologically active. In the case of IL-1 β , this cleavage involves an intracellular cysteine protease, known as ICE, which is required to release the active fragment from the inactive precursor. The precursor of IL-1 α is active.

These two proteins act by binding to cell surface receptors found on almost all cell types and triggering a range of responses either alone or in concert with other secreted factors. These range from effects on proliferation (e.g. fibroblasts, T cells) apoptosis (e.g. A375 melanoma cells), cytokine induction (e.g. of TNF, IL-1, IL-8), receptor activation (e.g. E-selectin), eicosanoid production (e.g. PGE2) and the secretion of degradative enzymes (e.g. collagenase). To achieve these effects, IL-1 activates transcription factors such as NF-KB and AP-1. Several of the activities of IL-1 action on target cells are believed to be mediated through activation of kinase cascades that have also been associated with cellular stresses, such as the stress activated MAP kinase JNK/SAPK and p38.

A third member of the IL-1 family was subsequently discovered which acts as a natural antagonist of IL-1 α and IL-1 β by binding to the IL-1 receptor but not transducing an intracellular signal or a biological response. The protein is called IL-1Ra (for IL-1 receptor antagonist) or IRAP (for IL-1 receptor antagonist protein). At least three alternatively spliced forms of IL-1Ra exist: one encodes secreted protein, and the other two encode intracellular proteins. IL-1 α , IL-1 β and IL-1Ra exhibit approximately 25-30% sequence identity with each other and share a similar three dimensional structure consisting of twelve β -strands folded into a β -barrel, with an internal thrice repeated structural motif.

There are three known IL-1 receptor subunits. The active receptor complex consists of the type I receptor and IL-1 accessory protein (IL-1RAcP). The type I receptor is responsible for binding of the IL-1 α , IL-1 β and IL-1Ra ligands, and is able to do so in the absence of the IL-1RAcP. However, signal transduction requires the interaction of IL-1 α or IL-1 β

with the IL-1RAcP. IL-1Ra does not interact with the IL-1RAcP and hence cannot induce signal transduction. A third receptor subunit, the type II receptor, binds IL-1 α and IL-1 β but cannot transduce signal due its lack of an intracellular domain. Instead, the type II receptor either acts as a decoy in its membrane bound form or as an IL-1 antagonist in a processed, secreted form, and hence inhibits IL-1 activity. The type II receptor weakly binds to IL-1Ra.

Many studies using IL-1Ra, soluble IL-1R derived from the extracellular domain of the type I IL-1 receptor, antibodies to IL-1 α or IL-1 β , and transgenic knockout mice for these genes have shown that IL-1 plays a role in a number of pathophysiologies (for a review, see Dinarello, Blood, 87: 2095-2147 (1996)). For example, IL-1Ra has been shown to be effective in animal models of septic shock, rheumatoid arthritis, graft-versus-host disease (GVHD), stroke, cardiac ischemia, psoriasis, inflammatory bowel disease, and asthma. In addition, IL-1Ra has demonstrated efficacy in clinical trials for rheumatoid arthritis and GVHD, and is also in clinical trials for inflammatory bowel disease, asthma and psoriasis.

More recently, interleukin-18 (IL-18) was placed in the IL-1 family (for a review, see Dinarello et al, J. Leukocyte Biol., 63: 658-664 (1998)). IL-18 shares the β -pleated, barrel-like form of IL-1 α and IL-1 β . In addition, IL-18 is the natural ligand for the IL-1 receptor family member formerly known as IL-1R-related protein (IL-1Rrp) (now known as the IL-18 receptor (IL-18R)). IL-18 has been shown to initiate the inflammatory cytokine cascade in a mixed population of peripheral blood mononuclear cells (PBMCs) by triggering the constitutive IL-18 receptors on lymphocytes and NK cells, inducing TNF production in the activated cells. TNF, in turn, stimulates IL-1 and IL-8 production in CD14+ cells. Because of its ability to induce TNF, IL-1, and both C-C and C-X-C chemokines, and because IL-18 induces Fas ligand as well as nuclear translocation of nuclear factor κ B (NF- κ B), IL-18 ranks with other pro-inflammatory cytokines as a likely contributor to systemic and local inflammation.

SUMMARY OF THE INVENTION

A family of cDNA clones (DNA85066, DNA96786, DNA94618, DNA92929, DNA96787, and DNA92505) has been identified, having homology to interleukin-1, that encode novel polypeptides, designated in the present application as "interleukin-1-like polypeptides" or "IL-1lp".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding an IL-1lp polypeptide.

In one aspect, the isolated nucleic acid comprises DNA encoding an IL-1lp polypeptide that retains at least one biologic activity of a native sequence IL-1lp, which DNA has at least about 80% sequence identity, or at least about 85% sequence identity, or at least about 90% sequence identity, or at least about 95% sequence identity to (a) a DNA molecule selected from the group consisting of: (1) a DNA molecule encoding an IL-1lp polypeptide having amino acid residues from at or about 37 to at or about 203, inclusive of Figure 2 (SEQ ID NO:), (2) a DNA molecule encoding an IL-1lp polypeptide having amino acid residues from at or about 15 to at or about 193, inclusive of Figure 3 (SEQ ID NO:), (3) amino acid residues from at or about 34 to at or about 155, inclusive of Figure 7 (SEQ ID NO:), and (4) amino acid residues from at or about 34 to at or about 155, inclusive of Figure 9 (SEQ ID NO:), or (b) the complement of the DNA molecule of (a).

In another aspect, the invention concerns an isolated nucleic acid molecule encoding an IL-1lp polypeptide

comprising DNA having at least 90 nucleotides and hybridizing to the complement of a nucleic acid sequence selected from the group consisting of: (1) the nucleic acid sequence consisting of nucleotide positions from at or about 145 to at or about 180 in the sense strand of Figure 3 (SEQ ID NO:); (2) the nucleic acid sequence consisting of nucleotide positions from at or about 238 to at or about 465 in the sense strand of Figure 7 (SEQ ID NO:); and (3) the nucleic acid sequence consisting of nucleotide positions from at or about 424 to at or about 609 in the sense strand of Figure 9 (SEQ ID NO:). Preferably, hybridization occurs under stringent hybridization and wash conditions.

In another aspect, the invention concerns an isolated nucleic acid molecule comprising DNA encoding an IL-11p polypeptide that retains at least one biologic activity of a native sequence IL-11p, which DNA hybridizes to the complement of a nucleic acid sequence selected from the group consisting of: (1) the nucleic acid sequence consisting of nucleotide positions from about 118 to about 618 in the sense strand of Figure 2 (SEQ ID NO:); (2) the nucleic acid sequence consisting of nucleotide positions from about 145 to about 681 in the sense strand of Figure 3 (SEQ ID NO:); (3) the nucleic acid sequence consisting of nucleotide positions from about 100 to about 465 in the sense strand of Figure 7 (SEQ ID NO:); and (4) the nucleic acid sequence consisting of nucleotide positions from about 244 to about 609 in the sense strand of Figure 9 (SEQ ID NO:). Preferably, hybridization occurs under stringent hybridization and wash conditions.

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising DNA encoding an IL-11p polypeptide that retains at least one biologic activity of a native sequence IL-11p, which DNA has at least about 80% sequence identity, or at least about 85% sequence identity, or at least about 90% sequence identity, or at least about 95% sequence identity to (a) a DNA encoding the same mature polypeptide encoded by the human protein cDNA in ATCC Deposit No. _____ (DNA85066-P2534), ATCC Deposit No. _____ (DNA96786-P2534), ATCC Deposit No. _____ (DNA96787-P2534), or ATCC Deposit No. _____ (DNA92505-P2534), or (b) the complement of the DNA molecule of (a). In a preferred embodiment, the nucleic acid comprises a DNA encoding the same mature polypeptide encoded by the human protein cDNA in ATCC Deposit No. _____ (DNA85066-P2534), ATCC Deposit No. _____ (DNA96786-P2534), ATCC Deposit No. _____ (DNA92929-P2534), ATCC Deposit No. _____ (DNA96787-P2534), or ATCC Deposit No. _____ (DNA92505-P2534).

In a still further aspect, the invention concerns an isolated nucleic acid molecule comprising (a) DNA encoding an IL-11p polypeptide that retains at least one biologic activity of a native sequence IL-11p and that has at least about 80% sequence identity, or at least about 85% sequence identity, or at least about 90% sequence identity, or at least about 95% sequence identity to an amino acid sequence selected from the group consisting of: (1) amino acid residues from at or about 37 to at or about 203, inclusive of Figure 2 (SEQ ID NO:); (2) amino acid residues from at or about 15 to at or about 193, inclusive of Figure 3 (SEQ ID NO:); (3) amino acid residues from at or about 34 to at or about 155, inclusive of Figure 7 (SEQ ID NO:); and (4) amino acid residues from at or about 34 to at or about 155, inclusive of Figure 9 (SEQ ID NO:), or the complement of the DNA of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule having at least 300 nucleotides and comprising DNA encoding an IL-11p that retains at least one biologic activity of a native sequence IL-11p, which DNA is produced by hybridizing a test DNA molecule under stringent conditions with (a) a DNA molecule encoding an IL-11p

polypeptide selected from the group consisting of: (1) an IL-11p polypeptide having the sequence of amino acid residues from at or about 37 to at or about 203, inclusive of Figure 2 (SEQ ID NO:), (2) an IL-11p polypeptide having the sequence of amino acid residues from at or about 15 to at or about 193, inclusive of Figure 3 (SEQ ID NO:), (3) an IL-11p polypeptide having the sequence of amino acid residues from at or about 34 to at or about 155, inclusive of Figure 7 (SEQ ID NO:), and (4) an IL-11p polypeptide having the sequence of amino acid residues from at or about 34 to at or about 155, inclusive of Figure 9 (SEQ ID NO:), or (b) the complement of the DNA molecule of (a), and, if the test DNA molecule encodes an IL-11p that retains at least one biologic activity of a native sequence IL-11p and if the test DNA molecule has at least about an 80 % sequence identity, or at least about an 85% sequence identity, or at least about a 90% sequence identity, or at least about a 95% sequence identity to the DNA molecule of (a) or (b), isolating the test DNA molecule.

In a specific aspect, the invention provides an isolated nucleic acid molecule comprising DNA encoding an IL-11p polypeptide, with or without the N-terminal signal sequence and/or the initiating methionine, or is complementary to such encoding nucleic acid molecule. The signal peptide has been tentatively identified as extending from amino acid position 1 to at or about amino acid position 14 in the IL-11p sequence of Figure 3 (SEQ ID NO:), from amino acid position 1 to at or about amino acid position 26 in the IL-11p sequence of Figure 5 (SEQ ID NO:), from amino acid position 1 to at or about amino acid position 33 in the IL-11p sequence of Figure 7 (SEQ ID NO:), and from amino acid position 1 to at or about amino acid position 33 in the IL-11p sequence of Figure 9 (SEQ ID NO:).

In another aspect, the invention concerns an isolated nucleic acid molecule comprising (a) DNA encoding an IL-11p polypeptide that retains at least one biologic activity of a native sequence IL-11p and that scores at least about 80% positives, or at least about 85% positives, or at least about 90% positives, or at least about 95% positives when compared with an amino acid sequence selected from the group consisting of: (1) the amino acid sequence of residues from at or about 37 to at or about 203, inclusive of Figure 2 (SEQ ID NO:), (2) the amino acid sequence of residues from at or about 15 to at or about 193, inclusive of Figure 3 (SEQ ID NO:), (3) the amino acid sequence of residues from at or about 34 to at or about 155, inclusive of Figure 7 (SEQ ID NO:), and (4) the amino acid sequence of residues from at or about 34 to at or about 155, inclusive of Figure 9 (SEQ ID NO:), or (b) the complement of the DNA of (a).

In another embodiment, the invention provides a vector comprising DNA encoding IL-11p or its variants. The vector may comprise any of the isolated nucleic acid molecules hereinabove defined.

A host cell comprising such a vector is also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing IL-11p polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of IL-11p and recovering IL-11p from the cell culture.

In another embodiment, the invention provides isolated IL-11p polypeptide encoded by any of the isolated nucleic acid sequences hereinabove defined.

In another aspect, the invention provides isolated native sequence IL-11p polypeptide, which in one embodiment, includes an amino acid sequence selected from the group consisting of: (1) the amino acid sequence of residues from at or about 37 to at or about 203, inclusive of Figure 2 (SEQ ID NO:), (2) the amino acid sequence of residues from at or about 15 to at or about 193, inclusive of Figure 3 (SEQ ID NO:), (3) the amino acid sequence of residues from at or about 34 to

at or about 155, inclusive of Figure 7 (SEQ ID NO:), and (4) the amino acid sequence of residues from at or about 34 to at or about 155, inclusive of Figure 9 (SEQ ID NO:).

In another aspect, the invention concerns an isolated IL-11p polypeptide that retains at least one biologic activity of a native sequence IL-11p and that consists of an amino acid sequence having at least about 80% sequence identity, or at least about 85% sequence identity, or at least about 90% sequence identity, or at least about 95% sequence identity to the sequence of amino acid residues from at or about 37 to at or about 203, inclusive of Figure 2 (SEQ ID NO:), the sequence of amino acid residues from at or about 15 to at or about 193, inclusive of Figure 3 (SEQ ID NO:), the sequence of amino acid residues from at or about 34 to at or about 155, inclusive of Figure 7 (SEQ ID NO:), or the sequence of amino acid residues from at or about 34 to at or about 155, inclusive of Figure 9 (SEQ ID NO:).

In a further aspect, the invention concerns an isolated IL-11p polypeptide that retains at least one biologic activity of a native sequence IL-11p and that consists of an amino acid sequence scoring at least about 80% positives, or at least about 85% positives, or at least about 90% positives, or at least about 95% positives when compared with an amino acid sequence selected from the group consisting of: (1) the amino acid sequence of residues from at or about 37 to at or about 203, inclusive of Figure 2 (SEQ ID NO:), (2) the amino acid sequence of residues from at or about 15 to at or about 193, inclusive of Figure 3 (SEQ ID NO:), (3) the amino acid sequence of residues from at or about 34 to at or about 155, inclusive of Figure 7 (SEQ ID NO:), and (4) the amino acid sequence of residues from at or about 34 to at or about 155, inclusive of Figure 9 (SEQ ID NO:).

In yet another aspect, the invention concerns an isolated IL-11p polypeptide comprising an amino acid sequence selected from the group consisting of: (1) amino acid residues from about 37 to about 63 of Figure 2 (SEQ ID NO:); (2) amino acid residues from about 15 to about 53 of Figure 3 (SEQ ID NO:); (3) amino acid residues from about 80 to about 155 of Figure 7 (SEQ ID NO:); and (4) amino acid residues from about 95 to about 155 of Figure 9 (SEQ ID NO:), or a fragment of such IL-11p polypeptide that coincides with a stretch of at least about 10 contiguous amino acids in such amino acid sequence, wherein the IL-11p polypeptide or fragment thereof is sufficient to provide a binding site for an anti-IL-11p antibody. Preferably, the IL-11p fragment retains at least one biologic activity of a native sequence IL-11p polypeptide.

In a still further aspect, the invention provides a polypeptide that is produced by (i) hybridizing a test DNA molecule under stringent conditions with (a) a DNA molecule encoding an amino acid sequence selected from the group consisting of: (1) amino acid residues from at or about 37 to at or about 203, inclusive of Figure 2 (SEQ ID NO:), (2) amino acid residues from at or about 15 to at or about 193, inclusive of Figure 3 (SEQ ID NO:), (3) amino acid residues from at or about 34 to at or about 155, inclusive of Figure 7 (SEQ ID NO:), and (4) amino acid residues from at or about 34 to at or about 155, inclusive of Figure 9 (SEQ ID NO:), or (b) the complement of the DNA molecule of (a), and if the test DNA molecule encodes an IL-11p polypeptide that retains at least one biologic activity of a native sequence IL-11p and if the test DNA molecule has at least about an 80% sequence identity, or at least about an 85% sequence identity, or at least about a 90% sequence identity, or at least about a 95% sequence identity to the DNA molecule of (a) or (b), (ii) culturing a host cell comprising the test DNA molecule under conditions suitable for expression of the IL-11p polypeptide, and (iii) recovering the IL-11p polypeptide from the cell culture.

In another embodiment, the invention provides chimeric molecules comprising an IL-11p polypeptide fused to a heterologous polypeptide or amino acid sequence. An example of such a chimeric molecule comprises an IL-11p polypeptide fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which specifically binds to an IL-11p polypeptide.

Optionally, the antibody is a monoclonal antibody.

In yet another embodiment, the invention concerns agonists and antagonists of a native IL-11p polypeptide. In a particular embodiment, the agonist or antagonist is an anti-IL-11p antibody.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists of a native IL-11p polypeptide, by contacting the native IL-11p polypeptide with a candidate molecule and monitoring a biological activity mediated by said polypeptide.

In a still further embodiment, the invention concerns a composition comprising an IL-11p polypeptide, or an agonist or antagonist as hereinabove defined, in combination with a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:) and derived amino acid sequences (SEQ ID NOS: __-__) related to a native sequence hIL-1Ra1. The nucleotide sequence (SEQ ID NO:) contains an intron believed to extend from nucleotide positions 181 to 432, with a splice donor site at nucleotide positions 181 to 186 and splice acceptor site at nucleotide positions 430 to 432. The amino acid sequences (SEQ ID NOS: __ and __) are derived from the exonic sequences that are believed to make up the processed (intron-free) coding sequence.

Figure 2 shows the nucleotide sequence (SEQ ID NO:) and derived amino acid sequence (SEQ ID NO:) of a native sequence hIL-1Ra1 polypeptide fused at its N-terminus to a heterologous signal peptide (amino acid positions 1-15), flag peptide affinity handle (amino acid positions 16-23) and peptide linker (amino acid positions 24-36).

Figure 3 shows the nucleotide sequence (SEQ ID NO:) and derived amino acid sequence (SEQ ID NO:) of a native sequence hIL-1Ra1 polypeptide. The nucleotide sequence (SEQ ID NO:) and derived amino acid sequence (SEQ ID NO:) are believed to represent the processed (intron-free) form and intact hIL-1Ra1 polypeptide, respectively, of the nucleotide sequence (SEQ ID NO:) and amino acid sequences (SEQ ID NOS: __-__) of Figure 1. The start and stop codons in the coding sequence are located at nucleotide positions 103-105 and 682-684, respectively. The putative signal sequence extends from amino acid positions 1 to 14. A putative cAMP- and cGMP-dependent protein kinase phosphorylation site is located at amino acid positions 33-36. Putative N-myristoylation sites are located at amino acid positions 50-55 and 87-92.

Figure 4 shows the nucleotide sequence (SEQ ID NO:) of EST AI014548.

Figure 5 shows the nucleotide sequence (SEQ ID NO:) and derived amino acid sequence (SEQ ID NO:) of a native sequence hIL-1Ra2 polypeptide. The start and stop codons in the coding sequence are located at nucleotide positions 96-98 and 498-500, respectively. The putative signal sequence extends from amino acid positions 1-26.

Figure 6 shows the nucleotide sequence (SEQ ID NO:) of EST 1433156.

Figure 7 shows the nucleotide sequence (SEQ ID NO:) and derived amino acid sequence (SEQ ID NO:) of a native sequence hIL-1Ra3 polypeptide. The start and stop codons in the coding sequence are located at nucleotide positions 1-3 and 466-468, respectively. The putative signal sequence extends from amino acid positions 1-33. Putative N-myristoylation sites are located at amino acid positions 29-34, 30-35, 60-65, 63-68, 73-78, 91-96 and 106-111. An interleukin-1-like sequence is located at amino acid positions 111-131.

Figure 8 shows the nucleotide sequence (SEQ ID NO:) of EST 5120028.

Figure 9 shows the nucleotide sequence (SEQ ID NO:) and derived amino acid sequence (SEQ ID NO:) of a native sequence mIL-1Ra3 polypeptide. The start and stop codons in the coding sequence are located at nucleotide positions 145-147 and 610-612, respectively. The putative signal sequence extends from amino acid positions 1-33. Putative N-myristoylation sites are located at amino acid positions 29-34, 60-65, 63-68, 91-96 and 106-111. An interleukin-1-like sequence is located at amino acid positions 111-131.

Figure 10 shows the nucleotide sequence (SEQ ID NO:) of EST AA030324.

Figure 11 is an autoradiograph of Northern blots depicting expression of hIL-1Ra3 mRNA in placental tissue and expression of mIL-1Ra3 mRNA in day-17 mouse embryo tissue.

Figure 12 is an amino acid sequence alignment of native sequence hIL-1Ra1, hIL-1Ra2, hIL-1Ra3 and mIL-1Ra3 polypeptides with known proteins hIL-1Ra and hIL-1Ra β .

Figure 13 is a Western blot depicting the interleukin-18 receptor (IL-18R) binding activity of hIL-1Ra1. In the top panel (depicting a protein band at approximately 22 kD), a conditioned medium containing FLAGhIL-1Ra1 and FLAGIL-1R-ECD-Fc (shown in the left lane) and a conditioned medium containing FLAGhIL-1Ra1 and FLAGIL-18R-ECD-Fc (shown in the right lane) were each immunoprecipitated with protein G-sepharose, and the resulting precipitates were resolved by gel electrophoresis and Western blotting with anti-FLAG monoclonal antibody. In the middle and bottom panels (depicting protein bands at approximately 22 kD and 85 kD), a second aliquot from the FLAGhIL-1Ra1 and FLAGIL-1R-ECD-Fc conditioned medium used in the top panel (shown in the left lane) and a second aliquot from the FLAGhIL-1Ra1 and FLAGIL-18R-ECD-Fc conditioned medium used in the top panel (shown in the right lane) were each immunoprecipitated with anti-FLAG monoclonal antibody, and the resulting precipitates were resolved by gel electrophoresis and Western blotting with anti-FLAG monoclonal antibody.

Figure 14 is a Western blot depicting the interleukin-1 receptor (IL-1R) binding activity of mIL-1Ra3. In the top panel (depicting a protein band at approximately 21 kD) and the bottom panel (depicting protein bands at approximately 85 kD) the FLAGIL-1R-ECD-Fc in conditioned medium (shown in the left lane) and the FLAGIL-18R-ECD-Fc in conditioned medium (shown in the right lane) were immobilized with protein G-agarose, the resulting solid phase was contacted with conditioned medium containing FLAGmIL-1Ra3, and the resulting bound complexes were resolved by gel electrophoresis and Western blotting with anti-FLAG monoclonal antibody.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions:

The terms "interleukin-1-like polypeptide", "interleukin-1-like protein", "IL-1lp", "IL-1lp polypeptide", and "IL-1lp protein" encompass any native sequence IL-1lp, and further encompass IL-1lp variants (which are further defined herein). The IL-1lp may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant and/or synthetic methods.

5 A "native sequence IL-1lp" comprises a polypeptide having the same amino acid sequence as a native sequence hIL-1Ra1, hIL-1Ra2, hIL-1Ra3, or mL-1Ra3, (which are further defined herein). Such native sequence IL-1lp can be isolated from nature or can be produced by recombinant and/or synthetic means. The term "native sequence IL-1lp" specifically encompasses naturally-occurring truncated or secreted forms (e.g., a processed, mature sequence) and naturally-occurring allelic variants of the IL-1lp.

10 The terms "naturally-occurring amino acid sequence" and "native amino acid sequence" mean any amino acid sequence found in a polypeptide existing in nature, i.e. present in a naturally-occurring polypeptide.

The terms "non-naturally-occurring amino acid sequence" and "non-native amino acid sequence" mean any amino acid sequence not found in a polypeptide existing in nature, i.e. not present in a naturally-occurring polypeptide.

"IL-1lp variant" is defined as any polypeptide that comprises a variant of hIL-1Ra1, hIL-1Ra2, hIL-1Ra3, or mL-1Ra3 (which are further defined herein).

15 Human interleukin-1 receptor antagonist analog 1 ("hIL-1Ra1"), hIL-1Ra1 polypeptide, and hIL-1Ra1 protein are defined as any native sequence hIL-1Ra1 or variant hIL-1Ra1.

A "native sequence hIL-1Ra1" means a polypeptide comprising a naturally-occurring amino acid sequence selected from the group consisting of: (1) the amino acid sequence of amino acid residues from at or about 37 to at or about 63 of Figure 2 (SEQ ID NO:); (2) the amino acid sequence of amino acid residues from at or about 37 to at or about 203 of Figure 2 (SEQ ID NO:); (3) the amino acid sequence of amino acid residues from at or about 15 to about 53 of Figure 3 (SEQ ID NO:); (4) the amino acid sequence of amino acid residues from at or about 15 to at or about 193 of Figure 3 (SEQ ID NO:); and (5) the amino acid sequence of any naturally-occurring truncated or secreted form or any naturally-occurring allelic variant of a polypeptide comprising the amino acid sequences of (1) or (2) or (3) or (4). In one embodiment of the invention, the native sequence hIL-1Ra1 is a mature or full-length native sequence hIL-1Ra1 comprising amino acids from at or about 37 to at or about 203 of Figure 2 (SEQ ID NO:) or amino acids from at or about 15 to at or about 193 of Figure 3 (SEQ ID NO:).

"hIL-1Ra1 variant" is defined as any hIL-1Ra1 N-terminal variant or hIL-1Ra1 full sequence variant (which are further defined herein).

30 "hIL-1Ra1 N-terminal variant" means any hIL-1Ra1 other than a native sequence hIL-1Ra1, which variant is an active hIL-1Ra1, as defined below, having at least about 80% amino acid sequence identity with an amino acid sequence selected from the group consisting of: (1) the amino acid sequence of amino acid residues from at or about 37 to at or about 63 of Figure 2 (SEQ ID NO:); and (2) the amino acid sequence of amino acid residues from at or about 15 to at or about 53 of Figure 3 (SEQ ID NO:). Such hIL-1Ra1 N-terminal variants include, for instance, hIL-1Ra1 polypeptides wherein one or more amino acid residues are added, or deleted, internally or at the N- or C-terminus, of the sequence of amino acid

residues from at or about 37 to at or about 63 of Figure 2 (SEQ ID NO:) or amino acid residues from at or about 15 to at or about 53 of Figure 3 (SEQ ID NO:). Ordinarily, an hIL-1Ra1 N-terminal variant will have at least about 80% amino acid sequence identity, or at least about 85% amino acid sequence identity, or at least about 90% amino acid sequence identity, or at least about 95% amino acid sequence identity with an amino acid sequence selected from the group consisting of: (1) the amino acid sequence of amino acid residues from at or about 37 to at or about 63 of Figure 2 (SEQ ID NO:); and (2) the amino acid sequence of amino acid residues from at or about 15 to at or about 53 of Figure 3 (SEQ ID NO:).

"hIL-1Ra1 full sequence variant" means any hIL-1Ra1 other than a native sequence hIL-1Ra1, which variant retains at least one biologic activity of a native sequence hIL-1Ra1, such as the ability to bind IL-18R, and which variant has at least about 80% amino acid sequence identity, or at least about 85% amino acid sequence identity, or at least about 90% amino acid sequence identity, or at least about 95% amino acid sequence identity with an amino acid sequence selected from the group consisting of: (1) the amino acid sequence of amino acid residues from at or about 37 to at or about 203 of Figure 2 (SEQ ID NO:); and (2) the amino acid sequence of amino acid residues from at or about 15 to at or about 193 of Figure 3 (SEQ ID NO:). Such hIL-1Ra1 full sequence variants include, for instance, hIL-1Ra1 polypeptides wherein one or more amino acid residues are added, or deleted, internally or at the N- or C-terminus, of the sequence of amino acid residues from at or about 37 to at or about 203 of Figure 2 (SEQ ID NO:) or amino acid residues from at or about 15 to at or about 193 of Figure 3 (SEQ ID NO:).

Human interleukin-1 receptor antagonist analog 2 ("hIL-1Ra2"), hIL-1Ra2 polypeptide, and hIL-1Ra2 protein are defined as any native sequence hIL-1Ra2 or hIL-1Ra2 fusion variant (which are further defined herein).

A "native sequence hIL-1Ra2" means (1) a polypeptide comprising the amino acid sequence of amino acid residues from at or about 1 to at or about 134 of Figure 5 (SEQ ID NO:) or (2) a polypeptide consisting of a naturally-occurring truncated or secreted form of the polypeptide of (1). In one embodiment of the invention, the native sequence hIL-1Ra2 is a mature or full-length native sequence hIL-1Ra2 consisting of amino acids from at or about 27 to at or about 134 of Figure 5 (SEQ ID NO:).

"hIL-1Ra2 fusion variant" means a chimeric hIL-1Ra2 consisting of a native sequence hIL-1Ra2 fused at its N-terminus or C-terminus to a heterologous amino acid or amino acid sequence. In one embodiment, the hIL-1Ra2 fusion variant polypeptide consists of a native sequence of hIL-1Ra2 fused at its N-terminus or C-terminus to a heterologous amino acid or amino acid sequence, wherein the heterologous amino acid or amino acid sequence is heterologous to the native sequence, i.e. the resulting chimeric sequence is non-naturally occurring. In another embodiment, the hIL-1Ra2 variant consists of the amino acid sequence of amino acids from at or about 27 to at or about 134 of Figure 5 (SEQ ID NO:) fused at its N-terminus or C-terminus to a heterologous amino acid or amino acid sequence to form a non-naturally occurring fusion protein. Such hIL-1Ra2 fusion variants include, for instance, hIL-1Ra2 polypeptides wherein a heterologous secretion leader sequence is fused to the N-terminus of the mature, full-length hIL-1Ra2 sequence of amino acids from at or about 27 to at or about 134 of Figure 5 (SEQ ID NO:).

Human interleukin-1 receptor antagonist analog 3 ("hIL-1Ra3"), hIL-1Ra3 polypeptide, and hIL-1Ra3 protein are defined as any native sequence hIL-1Ra3 or variant hIL-1Ra3 (which are further defined herein).

A "native sequence hIL-1Ra3" means a polypeptide comprising an amino acid sequence selected from the group consisting of: (1) the amino acid sequence of amino acid residues from at or about 95 to at or about 134 of Figure 7 (SEQ ID NO:); (2) the amino acid sequence of amino acid residues from at or about 34 to at or about 155 of Figure 7 (SEQ ID NO:); and (3) the amino acid sequence of any naturally-occurring truncated or secreted form or any naturally-occurring allelic variant of a polypeptide comprising the amino acid sequence of (1) or (2). In one embodiment of the invention, the native sequence hIL-1Ra3 is a mature or full-length native sequence hIL-1Ra3 comprising amino acids from at or about 34 to at or about 155 of Figure 7 (SEQ ID NO:).

"hIL-1Ra3 variant" is defined as any hIL-1Ra3 C-terminal variant or hIL-1Ra3 full sequence variant (which are further defined herein).

"hIL-1Ra3 C-terminal variant" means any hIL-1Ra3 other than a native sequence hIL-1Ra3, which variant is an active hIL-1Ra3, as defined below, having at least about 80% amino acid sequence identity with the amino acid sequence of amino acid residues from at or about 95 to at or about 134 of Figure 7 (SEQ ID NO:) or the amino acid sequence of amino acid residues from at or about 80 to at or about 155 of Figure 7 (SEQ ID NO:). Such hIL-1Ra3 C-terminal variants include, for instance, hIL-1Ra3 polypeptides wherein one or more amino acid residues are added, or deleted, internally or at the N- or C-terminus, of the sequence of amino acid residues from at or about 95 to at or about 134 of Figure 7 (SEQ ID NO:) or the sequence of amino acid residues from at or about 80 to at or about 155 of Figure 7 (SEQ ID NO:). Ordinarily, an hIL-1Ra3 C-terminal variant will have at least about 80% amino acid sequence identity, or at least about 85% amino acid sequence identity, or at least about 90% amino acid sequence identity, or at least about 95% amino acid sequence identity with the amino acid sequence of amino acid residues from at or about 95 to at or about 134 of Figure 7 (SEQ ID NO:) or the amino acid sequence of amino acid residues from at or about 80 to at or about 155 of Figure 7 (SEQ ID NO:).

"hIL-1Ra3 full sequence variant" means any hIL-1Ra3 other than a native sequence hIL-1Ra3, which variant retains at least one biologic activity of a native sequence hIL-1Ra3, such as the ability to bind IL-1R, and which variant has at least about 80% amino acid sequence identity, or at least about 85% amino acid sequence identity, or at least about 90% amino acid sequence identity, or at least about 95% amino acid sequence identity with the amino acid sequence of amino acid residues from at or about 34 to at or about 155 of Figure 7 (SEQ ID NO:). Such hIL-1Ra3 full sequence variants include, for instance, hIL-1Ra3 polypeptides wherein one or more amino acid residues are added, or deleted, internally or at the N- or C-terminus, of the sequence of amino acid residues from at or about 34 to at or about 155 of Figure 7 (SEQ ID NO:).

Murine interleukin-1 receptor antagonist analog 3 ("mIL-1Ra3"), mIL-1Ra3 polypeptide, and mIL-1Ra3 protein are defined as any native sequence mIL-1Ra3 or variant mIL-1Ra3.

A "native sequence mIL-1Ra3" means a polypeptide comprising an amino acid sequence amino selected from the group consisting of: (1) the amino acid sequence of amino acid residues from at or about 95 to at or about 134 of Figure 9 (SEQ ID NO:); (2) the amino acid sequence of amino acid residues from at or about 34 to at or about 155 of Figure 9 (SEQ ID NO:); and (3) the amino acid sequence of any naturally-occurring truncated or secreted form or naturally-occurring allelic variants of a polypeptide comprising the amino acid sequence of (1) or (2). In one embodiment of the invention, the native

sequence mIL-1Ra3 is a mature or full-length native sequence mIL-1Ra3 comprising amino acids from at or about 34 to at or about 155 of Figure 9 (SEQ ID NO:).

"mIL-1Ra3 variant" is defined as any mIL-1Ra3 C-terminal variant or mIL-1Ra3 full sequence variant (which are further defined herein).

"mIL-1Ra3 C-terminal variant" means any mIL-1Ra3 other than a native sequence mIL-1Ra3, which variant is an active mIL-1Ra3, as defined below, having at least about 80% amino acid sequence identity with the amino acid sequence of amino acids from at or about 95 to at or about 134 of Figure 9 (SEQ ID NO:). Such mIL-1Ra3 C-terminal variants include, for instance, mIL-1Ra3 polypeptides wherein one or more amino acid residues are added, or deleted, internally or at the N- or C-terminus, of the sequence of amino acids from at or about 95 to at or about 134 of Figure 9 (SEQ ID NO:).

Ordinarily, an mIL-1Ra3 C-terminal variant will have at least about 80% amino acid sequence identity, or at least about 85% amino acid sequence identity, or at least about 90% amino acid sequence identity, and or at least about 95% amino acid sequence identity with the amino acid sequence of amino acids 95 to 134 of Figure 9 (SEQ ID NO:).

"mIL-1Ra3 full sequence variant" means any mIL-1Ra3 other than a native sequence mIL-1Ra3, which variant retains at least one biologic activity of a native sequence mIL-1Ra3, such as the ability to bind IL-1R, and which variant has at least about 85% amino acid sequence identity, or at least about 90% amino acid sequence identity, or at least about 95% sequence identity with the amino acid sequence of amino acid residues from at or about 34 to at or about 155 of Figure 9 (SEQ ID NO:). Such mIL-1Ra3 full sequence variants include, for instance, mIL-1Ra3 polypeptides wherein one or more amino acid residues are added, or deleted, internally or at the N- or C-terminus, of the sequence of amino acid residues from at or about 34 to at or about 155 of Figure 9 (SEQ ID NO:).

Human interleukin-1 receptor antagonist analog ("hIL-1Ra"), hIL-1Ra polypeptide, and hIL-1Ra protein are defined as any hIL-1Ra1, hIL-1Ra2 or hIL-1Ra3 polypeptide.

"Native sequence hIL-1Ra" comprises a polypeptide having the same amino acid sequence as a native sequence hIL-1Ra1, hIL-1Ra2, or hIL-1Ra3.

"hIL-1Rp variant" is defined as any polypeptide that comprises a variant of hIL-1Ra1, hIL-1Ra2, or hIL-1Ra3.

"Interleukin-1 receptor", "interleukin-1 receptor polypeptide", "interleukin-1 receptor protein", "IL-1 receptor", "IL-1R", "IL-1R polypeptide", and "IL-1R protein", are defined as the family of cell surface proteins that bind to interleukin-1 (IL-1) and/or function in IL-1-induced signal transduction in a given species, such as human or mouse.

"Interleukin-18 receptor", "interleukin-18 receptor polypeptide", "interleukin-18 receptor protein", "IL-18 receptor", "IL-18R", "IL-18R polypeptide", and "IL-18R protein", are defined as the family of cell surface proteins that bind to interleukin-18 (IL-18) and/or function in IL-18-induced signal transduction in a given species, such as human or mouse. IL-18R includes the IL-1 receptor related protein (IL-1Rrp) described in Torigoe et al., *J. Biol. Chem.*, 272: 25737-25742 (1997) and the IL-18 receptor accessory protein-like molecule (IL-18RAcPL) described in Born et al., *J. Biol. Chem.*, 273: 29445-29450 (1998).

"Interleukin-1-like family" and "IL-1-like family" are used to indicate the family of polypeptides related to the ligands of IL-1R or IL-18R. The IL-1-like family includes IL-1 receptor agonists and antagonists and related polypeptides

such as IL-1 α (described in Bazan et al., Nature, 379: 591 (1996), IL-1 β (Bazan et al.), IL-18 (interferon- γ inducing factor)(IGIF)(Bazan et al.), IL-1 receptor antagonist polypeptides such as secretory IL-1Ra (sIL-1Ra)(described in Eisenberg et al., Nature, 343: 341-346 (1990) and intracellular IL-1Ra (icIL-1Ra) (described in Haskill et al. , Proc. Natl. Acad. Sci. (USA), 88: 3681-3685 (1991)), and the IL-1lp polypeptides of the invention.

"Percent (%) amino acid sequence identity" with respect to the IL-1lp sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the IL-1lp sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. The % identity values used herein can be generated by WU-BLAST-2 which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996).

WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity.

The term "positives", in the context of sequence comparison performed as described above, includes residues in the sequences compared that are not identical but have similar properties (e.g. as a result of conservative substitutions). The % value of positives is determined by the fraction of residues scoring a positive value in the BLOSUM 62 matrix divided by the total number of residues in the aligned region.

In a similar manner, "percent (%) nucleic acid sequence identity" with respect to the coding sequence of the IL-1lp polypeptides identified herein is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues in the IL-1lp coding sequence. The identity values used herein can be generated by the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the IL-1lp natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" nucleic acid molecule encoding a IL-1lp polypeptide is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the IL-1lp-encoding nucleic acid. An isolated IL-1lp-encoding nucleic acid molecule is other than in the form or setting in

which it is found in nature. Isolated nucleic acid molecules therefore are distinguished from the IL-11p-encoding nucleic acid molecule as it exists in natural cells. However, an isolated nucleic acid molecule encoding a IL-11p polypeptide includes IL-11p-encoding nucleic acid molecules contained in cells that ordinarily express IL-11p where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

5 The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence.

10 For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

15 The term "antibody" is used in the broadest sense and specifically covers single anti-IL-11p monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies) and anti-IL-11p antibody compositions with polypeptidic specificity. The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

20 "Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel *et al.*, Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

30 "Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M

NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/mL denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising an IL-11p polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of IL-11p which retain one or more of the biologic activities of native or naturally-occurring IL-11p, or which exhibit immunological cross-reactivity with a native or naturally-occurring IL-11p.

As used herein, a "biologic activity" or "biological activity" of an IL-11p means any effector function exhibited by the IL-11p in the physiology or pathophysiology of a mammal, excluding any immunogenic or antigenic functions of the IL-11p. Immunogenic and antigenic functions of an IL-11p refer to the ability of the IL-11p to generate a humoral or cell-mediated immune response specific to the IL-11p, and the ability of the IL-11p to specifically recognize and interact with anti-IL-11p antibodies, B cells or T cells, respectively, in a mammal.

As used herein, "immunological cross-reactivity" with an IL-11p means that the candidate polypeptide is capable

of competitively inhibiting the binding of the IL-1p to polyclonal or monoclonal antibodies raised against the IL-1p.

In one embodiment, IL-1p activity includes the ability to agonize or antagonize one or more biological activities of any IL-1-like family member, e.g. an IL-1p activity that antagonizes an IL-1-mediated or IL-18-mediated inflammatory response. In another embodiment, IL-1p activity includes the ability to bind to the IL-18 receptor and/or IL-1 receptor.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native IL-1p polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native IL-1p polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native IL-1p polypeptides, peptides, small organic molecules, etc.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

The terms "inflammatory disorders" and "inflammatory diseases" are used interchangeably herein and refer to pathological states resulting in inflammation. Examples of such disorders include inflammatory skin diseases such as psoriasis and atopic dermatitis; systemic scleroderma and sclerosis; responses associated with inflammatory bowel disease (such as Crohn's disease and ulcerative colitis); ischemic reperfusion disorders including surgical tissue reperfusion injury, myocardial ischemic conditions such as myocardial infarction, cardiac arrest, reperfusion after cardiac surgery and constriction after percutaneous transluminal coronary angioplasty, stroke, and abdominal aortic aneurysms; cerebral edema secondary to stroke; cranial trauma; hypovolemic shock; asphyxia; adult respiratory distress syndrome; acute lung injury; Behcet's Disease; dermatomyositis; polymyositis; multiple sclerosis; dermatitis; meningitis; encephalitis; uveitis; osteoarthritis; autoimmune diseases such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis, and insulin-dependent diabetes mellitus (IDDM); diseases involving leukocyte diapedesis; central nervous system (CNS) inflammatory disorder; meningitis; multiple organ injury syndrome secondary to septicemia or trauma; inflammatory diseases of the liver, including alcoholic hepatitis and hepatic fibrosis; pathologic host responses to infection, including pathologic inflammation in granulomatous diseases, hepatitis, and bacterial pneumonia; antigen-antibody complex mediated diseases including glomerulonephritis; sepsis; sarcoidosis; immunopathologic responses to tissue/organ transplantation, including graft-versus host disease (GVHD); inflammations of the lung, including pleurisy,

alveolitis, vasculitis, pneumonia, chronic bronchitis, bronchiectasis, diffuse panbronchiolitis, hypersensitivity pneumonitis, idiopathic pulmonary fibrosis (IPF), and cystic fibrosis; inflammation in renal diseases, including acute or chronic nephritic conditions such as lupus nephritis; pancreatitis, etc. The preferred indications include rheumatoid arthritis, osteoarthritis, sepsis, acute lung injury, adult respiratory distress syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion (including surgical tissue reperfusion injury, stroke, myocardial ischemia, and acute myocardial infarction), asthma, psoriasis, graft-versus-host disease (GVHD), and inflammatory bowel disease such as ulcerative colitis.

As used herein, the terms "asthma", "asthmatic disorder", "asthmatic disease", and "bronchial asthma" refer to a condition of the lungs in which there is widespread narrowing of lower airways. "Atopic asthma" and "allergic asthma" refer to asthma that is a manifestation of an IgE-mediated hypersensitivity reaction in the lower airways, including, e.g., moderate or severe chronic asthma, such as conditions requiring the frequent or constant use of inhaled or systemic steroids to control the asthma symptoms. A preferred indication is allergic asthma.

II. Compositions and Methods of the Invention

A. Full-length IL-11p

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as IL-11p. In particular, cDNAs encoding IL-11p polypeptides have been identified and isolated, as disclosed in further detail in the Examples below.

Using WU-BLAST2 sequence alignment computer programs, it has been found that a full-length native sequence hIL-1Ra1 (shown in Figure 3 and SEQ ID NO:) has about 38% amino acid sequence identity with human IL-1 receptor antagonist beta (hIL-1Ra β), a full-length native sequence hIL-1Ra2 (shown in Figure 5 and SEQ ID NO:) has about 79% amino acid sequence identity with hIL-1Ra β , a full-length native sequence hIL-1Ra3 (shown in Figure 7 and SEQ ID NO:) has about 50% amino acid sequence identity with human intracellular IL-1 receptor antagonist (hICIL-1Ra), and a full-length native sequence mIL-1Ra3 (shown in Figure 9 and SEQ ID NO:) has about 49% amino acid sequence identity with mouse IL-1 receptor antagonist (mIL-1Ra) and has about 48% amino acid sequence identity with hICIL-1Ra. hIL-1Ra β is described in EP 0855404 published July 29, 1998. hICIL-1Ra is described in WO 95/10298 published April 20, 1995 and in Haskill et al., *Proc. Natl. Acad. Sci. (USA)*, **88**: 3681-3685 (1991). mIL-1Ra is described in Zahedi et al., *J. Immunol.*, **146**: 4228-4233 (1991), Matsushime et al., *Blood*, **78**: 616-623 (1991), Zahedi et al., *Cytokine*, **6**: 1-9 (1994), Eisenberg et al., *Proc. Natl. Acad. Sci. (USA)*, **88**: 5232-5236 (1991) and Shuck et al., *Eur. J. Immunol.*, **21**: 2775-2780 (1991). Accordingly, it is presently believed that the IL-11p polypeptides disclosed in the present application are newly identified members of the interleukin-1-like family and possess inflammatory or anti-inflammatory activities, or other cellular response activating or inhibiting activities, typical of the IL-1-like family.

B. IL-11p variants

In addition to the full-length native sequence IL-11p polypeptides described herein, it is contemplated that IL-11p

variants can be prepared. IL-11p variants can be prepared by introducing appropriate nucleotide changes into the IL-11p DNA, and/or by synthesis of the desired IL-11p polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the IL-11p, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence IL-11p or in various domains of the IL-11p described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the IL-11p that results in a change in the amino acid sequence of the IL-11p as compared with the native sequence IL-11p. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the IL-11p. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the IL-11p with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity in the *in vitro* assay described in the Examples below.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter *et al.*, *Nucl. Acids Res.*, 13:4331 (1986); Zoller *et al.*, *Nucl. Acids Res.*, 10:6487 (1987)], cassette mutagenesis [Wells *et al.*, *Gene*, 34:315 (1985)], restriction selection mutagenesis [Wells *et al.*, *Philos. Trans. R. Soc. London SerA*, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the IL-11p variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, *Science*, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, *The Proteins*, (W.H. Freeman & Co., N.Y.); Chothia, *J. Mol. Biol.*, 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of IL-11p

Covalent modifications of IL-11p are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an IL-11p polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the IL-11p. Derivatization with bifunctional agents

is useful, for instance, for crosslinking IL-11p to a water-insoluble support matrix or surface for use in the method for purifying anti-IL-11p antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionimide.

Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the IL-11p polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence IL-11p (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence IL-11p. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the IL-11p polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence IL-11p (for O-linked glycosylation sites). The IL-11p amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the IL-11p polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the IL-11p polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the IL-11p polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge *et al.*, *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of IL-11p comprises linking the IL-11p polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The IL-11p of the present invention may also be modified in a way to form a chimeric molecule comprising IL-11p

fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the IL-11p with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the IL-11p. The presence of such epitope-tagged forms of the IL-11p can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the IL-11p to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field *et al.*, *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan *et al.*, *Molecular and Cellular Biology*, 6:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky *et al.*, *Protein Engineering*, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp *et al.*, *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin *et al.*, *Science*, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner *et al.*, *J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth *et al.*, *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the IL-11p with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble form of an IL-11p polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

D. Preparation of IL-11p

The description below relates primarily to production of IL-11p by culturing cells transformed or transfected with a vector containing IL-11p nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare IL-11p. For instance, the IL-11p sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart *et al.*, *Solid-Phase Peptide Synthesis*, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, *J. Am. Chem. Soc.*, 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the IL-11p may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length IL-11p.

I. Isolation of DNA Encoding IL-11p

DNA encoding IL-11p may be obtained from a cDNA library prepared from tissue believed to possess the IL-11p mRNA and to express it at a detectable level. Accordingly, human IL-11p DNA can be conveniently obtained from a cDNA

library prepared from human tissue, such as described in the Examples. The IL-11p-encoding gene may also be obtained from a genomic library or by oligonucleotide synthesis.

Libraries can be screened with probes (such as antibodies to the IL-11p or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding IL-11p is to use PCR methodology [Sambrook *et al.*, *supra*; Dieffenbach *et al.*, *PCR Primer: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P -labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook *et al.*, *supra*.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined through sequence alignment using computer software programs such as BLAST, BLAST2, ALIGN, DNASTar, and INHERIT which employ various algorithms to measure homology.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook *et al.*, *supra*, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for IL-11p production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in *Mammalian Cell Biotechnology: A Practical Approach*, M. Butler, ed. (IRL Press, 1991) and Sambrook *et al.*, *supra*.

Methods of transfection are known to the ordinarily skilled artisan, for example, CaPO_4 and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook *et al.*, *supra*, or electroporation is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw *et al.*, *Gene*, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van

der Eb, *Virology*, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transformations have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen *et al.*, *J. Bact.*, 130:946 (1977) and Hsiao *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 76:3829 (1979).

However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, *e.g.*, polybrene, polymithine, may also be used. For various techniques for transforming mammalian cells, see Keown *et al.*, *Methods in Enzymology*, 185:527-537 (1990) and Mansour *et al.*, *Nature*, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635).

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for IL-11p-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism.

Suitable host cells for the expression of glycosylated IL-11p are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham *et al.*, *J. Gen Virol.*, 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.*, 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

The nucleic acid (*e.g.*, cDNA or genomic DNA) encoding IL-11p may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The IL-11p may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the

IL-1lp-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the C. *albicans* glucosylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the IL-1lp-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub *et al.*, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb *et al.*, *Nature*, 282:39 (1979); Kingsman *et al.*, *Gene*, 7:141 (1979); Tschemper *et al.*, *Gene*, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the IL-1lp-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang *et al.*, *Nature*, 275:615 (1978); Goeddel *et al.*, *Nature*, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer *et al.*, *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding IL-1lp.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzman *et al.*, *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess *et al.*, *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled

by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytrochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

IL-11p transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the IL-11p by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the IL-11p coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding IL-11p.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of IL-11p in recombinant vertebrate cell culture are described in Gething *et al.*, *Nature*, 293:620-625 (1981); Mantei *et al.*, *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or

polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence IL-11p polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to IL-11p DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of IL-11p may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of IL-11p can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify IL-11p from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the IL-11p. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, *Methods in Enzymology*, 182 (1990); Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular IL-11p produced.

E. Uses for IL-11p

Nucleotide sequences (or their complement) encoding IL-11p have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. IL-11p nucleic acid will also be useful for the preparation of IL-11p polypeptides by the recombinant techniques described herein.

The full-length native sequence IL-11p genes of Figure 1 (SEQ ID NO:), Figure 2 (SEQ ID NO:), Figure 3 (SEQ ID NO:), Figure 5, (SEQ ID NO:) Figure 7 (SEQ ID NO:) and Figure 9 (SEQ ID NO:), or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length IL-11p gene or to isolate still other genes (for instance, those encoding naturally-occurring variants of IL-11p or IL-11p from other species) which have a desired sequence identity to the IL-11p sequence disclosed in Figure 1 (SEQ ID NO:), Figure 2 (SEQ ID NO:), Figure 3 (SEQ ID NO:), Figure 5, (SEQ ID NO:) Figure 7 (SEQ ID NO:) or Figure 9 (SEQ ID NO:). Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from the nucleotide sequence of Figure 1 (SEQ ID NO:), Figure 2 (SEQ ID NO:), Figure 3 (SEQ ID NO:), Figure 5, (SEQ ID NO:) Figure 7 (SEQ ID NO:) or Figure 9 (SEQ ID NO:), or from genomic sequences including promoters, enhancer elements and introns of native sequence IL-11p. By way of example, a screening method will comprise isolating the coding region of the IL-11p gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ³²P or ³⁵S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the IL-11p gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the

probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related IL-11p coding sequences.

Nucleotide sequences encoding an IL-11p can also be used to construct hybridization probes for mapping the gene which encodes that IL-11p and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for IL-11p encode a protein which binds to another protein (example, where the IL-11p binds to an IL-1 receptor or IL-18 receptor), the IL-11p can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Screening assays can be designed to find lead compounds that mimic the biological activity of a native IL-11p or a receptor for IL-11p. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode IL-11p or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding IL-11p can be used to clone genomic DNA encoding IL-11p in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding IL-11p. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for IL-11p transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding IL-11p introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding IL-11p. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of IL-11p can be used to construct an IL-11p "knock out" animal which has a defective or altered gene encoding IL-11p as a result of homologous recombination between the endogenous gene encoding IL-11p and altered genomic DNA encoding IL-11p introduced into an embryonic cell of the animal. For example, cDNA

encoding IL-11p can be used to clone genomic DNA encoding IL-11p in accordance with established techniques. A portion of the genomic DNA encoding IL-11p can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the IL-11p polypeptide.

Nucleic acid encoding the IL-11p polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik et al., *Proc. Natl. Acad. Sci. USA* 83, 4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau et al., *Trends in Biotechnology* 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., *J. Biol. Chem.* 262, 4429-4432 (1987); and Wagner

et al., Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson *et al., Science* 256, 808-813 (1992).

The IL-1p polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the IL-1p product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions.

Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as Tween, Pluronic or PEG.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi *et al.*, Eds., Pergamon Press, New York 1989, pp. 42-96.

An "effective amount" of the IL-1p to be employed therapeutically will depend, for example, upon the therapeutic objectives, the route of administration, and the condition of the patient. Accordingly, it will be necessary for the therapist to titer the dosage and modify the route of administration as required to obtain the optimal therapeutic effect. Typically, the clinician will administer the IL-1p until a dosage is reached that achieves the desired effect. The progress of this therapy is easily monitored by conventional assays.

In one embodiment, the invention provides a method for treating an IL-1-mediated disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-1p, such as a native sequence IL-1p.

In another embodiment, the invention provides a method for treating an IL-1-mediated disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-1lp, such as a native sequence hIL-1lp, e.g. native sequence hIL-1Ra3.

In another embodiment, the invention provides a method for treating an IL-18-mediated disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-1lp, such as a native sequence IL-1lp.

In another embodiment, the invention provides a method for treating an IL-18-mediated disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-1lp, such as a native sequence hIL-1lp, e.g. native sequence hIL-1Ra1.

In one embodiment, the invention provides a method for treating an inflammatory disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-1lp, such as a native sequence IL-1lp.

In another embodiment, the invention provides a method for treating an inflammatory disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-1lp, such as a native sequence hIL-1lp, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating asthma comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-1lp, such as a native sequence IL-1lp.

In another embodiment, the invention provides a method for treating asthma comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-1lp, such as a native sequence hIL-1lp, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating rheumatoid arthritis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-1lp, such as a native sequence IL-1lp.

In another embodiment, the invention provides a method for treating rheumatoid arthritis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-1lp, such as a native sequence hIL-1lp, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating osteoarthritis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-1lp, such as a native sequence IL-1lp.

In another embodiment, the invention provides a method for treating osteoarthritis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-1lp, such as a native sequence hIL-1lp, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating sepsis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-1lp, such as a native sequence IL-1lp.

In another embodiment, the invention provides a method for treating sepsis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-1lp, such as a native sequence hIL-1lp, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating acute lung injury comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-11p, such as a native sequence IL-11p.

In another embodiment, the invention provides a method for treating acute lung injury comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-11p, such as a native sequence hIL-11p, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating adult respiratory distress syndrome comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-11p, such as a native sequence IL-11p.

In another embodiment, the invention provides a method for treating adult respiratory distress syndrome comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-11p, such as a native sequence hIL-11p, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating idiopathic pulmonary fibrosis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-11p, such as a native sequence IL-11p.

In another embodiment, the invention provides a method for treating idiopathic pulmonary fibrosis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-11p, such as a native sequence hIL-11p, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating an ischemic reperfusion disease, such as surgical tissue reperfusion injury, stroke, myocardial ischemia, or acute myocardial infarction, comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-11p, such as a native sequence IL-11p.

In another embodiment, the invention provides a method for treating an ischemic reperfusion disease, such as surgical tissue reperfusion injury, stroke, myocardial ischemia, or acute myocardial infarction, comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-11p, such as a native sequence hIL-11p, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating psoriasis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-11p, such as a native sequence IL-11p.

In another embodiment, the invention provides a method for treating psoriasis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-11p, such as a native sequence hIL-11p, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating graft-versus-host disease (GVHD) comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-11p, such as a native sequence IL-11p.

In another embodiment, the invention provides a method for treating graft-versus-host disease (GVHD) comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-11p, such as a native sequence hIL-11p, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

In another embodiment, the invention provides a method for treating an inflammatory bowel disease such as ulcerative colitis, comprising administering to a mammal, such as human, in need of such treatment an effective amount of an IL-11p, such as a native sequence IL-11p.

In another embodiment, the invention provides a method for treating an inflammatory bowel disease such as ulcerative colitis, comprising administering to a mammal, such as human, in need of such treatment an effective amount of an hIL-11p, such as a native sequence hIL-11p, e.g. native sequence hIL-1Ra1 or hIL-1Ra3.

F. Anti-IL-11p Antibodies

The present invention further provides anti-IL-11p antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

The anti-IL-11p antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the IL-11p polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

2. Monoclonal Antibodies

The anti-IL-11p antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the IL-11p polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include

hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Rockville, Maryland. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against IL-1p. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison *et al.*, *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain.

The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

The anti-IL-11p antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones *et al.*, *Nature*, 321: 522-525 (1986); Riechmann *et al.*, *Nature*, 332: 323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2: 593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones *et al.*, *Nature*, 321: 522-525 (1986); Riechmann *et al.*, *Nature*, 332: 323-327 (1988); Verhoeven *et al.*, *Science*, 239: 1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227: 381 (1991); Marks *et al.*, *J. Mol. Biol.*, 222: 581 (1991)]. The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner *et al.*, *J. Immunol.*, 147(1): 86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge,

human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *BioTechnology* 10, 779-783 (1992); Lonberg *et al.*, *Nature* 368: 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the IL-1p, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, *EMBO J.*, 10: 3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

G. Uses for anti-IL-11p Antibodies

The anti-IL-11p antibodies of the invention have various utilities. For example, anti-IL-11p antibodies may be used in diagnostic assays for IL-11p, e.g., detecting its expression in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, *Monoclonal Antibodies: A Manual of Techniques*, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter *et al.*, *Nature*, **144**: 945 (1962); David *et al.*, *Biochemistry*, **13**: 1014 (1974); Pain *et al.*, *J. Immunol. Meth.*, **40**: 219 (1981); and Nygren, *J. Histochem. and Cytochem.*, **30**: 407 (1982).

Anti-IL-11p antibodies also are useful for the affinity purification of IL-11p from recombinant cell culture or natural sources. In this process, the antibodies against IL-11p are immobilized on a suitable support, such as a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the IL-11p to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the IL-11p, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the IL-11p from the antibody.

In addition, anti-IL-11p antibodies are useful as therapeutic agents for targeting of native IL-11p in IL-11p-mediated disease conditions, e.g. disease states characterized by pathologic IL-1 or IL-18 agonist or agonist-like activity of the native IL-11p. In the treatment and prevention of a native IL-11p-mediated disorder with the anti-IL-11p antibody of the invention, the antibody composition will be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the antibody, the particular type of antibody, the method of administration, the scheduling of administration, and other factors known to medical practitioners. The "effective amount" or "therapeutically effective amount" of antibody to be administered will be governed by such considerations, and is the minimum amount necessary to prevent, ameliorate, or treat the native IL-11p-mediated disorder, including treating inflammatory diseases and reducing inflammatory responses. Such amount is preferably below the amount that is toxic to the host or renders the host significantly more susceptible to infections.

As a general proposition, the initial pharmaceutically effective amount of the antibody or antibody fragment administered parenterally per dose will be in the range of about 0.1 to 50 mg/kg of patient body weight per day, with the typical initial range of antibody used being 0.3 to 20 mg/kg/day, more preferably 0.3 to 15 mg/kg/day.

In one embodiment, using systemic administration, the initial pharmaceutically effective amount will be in the range of about 2 to 5 mg/kg/day.

For methods of the invention using administration by inhalation, the initial pharmaceutically effective amount will be in the range of about 1 microgram (μ g)/kg/day to 100 mg/kg/day.

In one embodiment, the invention provides a method for treating an IL-11p-mediated inflammatory disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

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In another embodiment, the invention provides a method for treating an hIL-11p-mediated inflammatory disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-1Ra1-mediated inflammatory disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

In another embodiment, the invention provides a method for treating an IL-11p-mediated asthmatic disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

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In another embodiment, the invention provides a method for treating an hIL-11p-mediated asthmatic disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-11Ra1-mediated asthmatic disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

In another embodiment, the invention provides a method for treating an IL-11p-mediated rheumatoid arthritic disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-11p-mediated rheumatoid arthritic disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-1Ra1-mediated rheumatoid arthritic disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

In another embodiment, the invention provides a method for treating an IL-11p-mediated osteoarthritic disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-11p-mediated osteoarthritic disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-1Ra1-mediated osteoarthritic disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

In another embodiment, the invention provides a method for treating an IL-11p-mediated septic disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-11p-mediated septic disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-1Ra1-mediated septic disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

In another embodiment, the invention provides a method for treating IL-11p-mediated acute lung injury comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

5 In another embodiment, the invention provides a method for treating hIL-11p-mediated acute lung injury comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

In another embodiment, the invention provides a method for treating hIL-1Ra1-mediated acute lung injury comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

10 In another embodiment, the invention provides a method for treating IL-11p-mediated adult respiratory distress syndrome comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

In another embodiment, the invention provides a method for treating hIL-11p-mediated adult respiratory distress syndrome comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

15 In another embodiment, the invention provides a method for treating hIL-1Ra1-mediated adult respiratory distress syndrome comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

In another embodiment, the invention provides a method for treating IL-11p-mediated idiopathic pulmonary fibrosis comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

20 In another embodiment, the invention provides a method for treating hIL-11p-mediated idiopathic pulmonary fibrosis comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

In another embodiment, the invention provides a method for treating hIL-1Ra1-mediated idiopathic pulmonary fibrosis comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

25 In another embodiment, the invention provides a method for treating an IL-11p-mediated ischemic reperfusion disease, such as surgical tissue reperfusion injury, stroke, myocardial ischemia, or acute myocardial infarction, comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-11p-mediated ischemic reperfusion disease, such as surgical tissue reperfusion injury, stroke, myocardial ischemia, or acute myocardial infarction, comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

30 In another embodiment, the invention provides a method for treating an hIL-1Ra1-mediated ischemic reperfusion disease, such as surgical tissue reperfusion injury, stroke, myocardial ischemia, or acute myocardial infarction, comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

In another embodiment, the invention provides a method for treating an IL-11p-mediated psoriatic disorder comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

35 In another embodiment, the invention provides a method for treating an hIL-11p-mediated psoriatic disorder

comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-1Ra1-mediated psoriatic disorder comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

5 In another embodiment, the invention provides a method for treating an IL-11p-mediated graft-versus-host disease (GVHD) comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

In another embodiment, the invention provides a method for treating an hIL-11p-mediated graft-versus-host disease (GVHD) comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

10 In another embodiment, the invention provides a method for treating an hIL-1Ra1-mediated graft-versus-host disease (GVHD) comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

In another embodiment, the invention provides a method for treating an IL-11p-mediated inflammatory bowel disease such as ulcerative colitis, comprising administering to a mammal, such as human, in need of such treatment an effective amount of an anti-IL-11p antibody.

15 In another embodiment, the invention provides a method for treating an hIL-11p-mediated inflammatory bowel disease such as ulcerative colitis, comprising administering to a human in need of such treatment an effective amount of an anti-hIL-11p antibody.

20 In another embodiment, the invention provides a method for treating an hIL-1Ra1-mediated inflammatory bowel disease such as ulcerative colitis, comprising administering to a human in need of such treatment an effective amount of an anti-hIL-1Ra1 antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

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EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1

Isolation of DNA encoding hIL-1Ra1 and mIL-1Ra3

A public expressed sequence tag (EST) DNA database (Genbank) was searched with human interleukin-1 receptor antagonist (hIL-1Ra) sequence, and the ESTs, designated AI014548 (Figure 4, SEQ ID NO: ____) and W08205 (Figure 10, SEQ ID NO: ____), were identified, which showed homology with the known protein hIL-1Ra.

EST clones AI014548 and W08205 were purchased from Research Genetics (Huntsville, AL) and the cDNA inserts were obtained and sequenced in their entirety.

The entire nucleotide sequence of the clone AI014548, designated DNA85066, is shown in Figure 1 (SEQ ID NO: ____). Clone DNA85066 contains a single open reading frame that is interrupted by an apparent intronic sequence. The intron is bounded by splice junctions at nucleotide positions 181 to 186 (splice donor site) and nucleotide positions 430 to 432 (splice acceptor site) (Fig. 1; SEQ ID NO: ____).

A virtual processed nucleotide sequence (Fig. 3; SEQ ID NO: ____), designated DNA94618, was derived by removing the apparent intronic sequence from clone DNA85066. Clone DNA94618 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 103-105, and a stop codon at nucleotide positions 682-684 (Fig. 3; SEQ ID NO: ____). The predicted polypeptide precursor (hIL-1Ra1) is 193 amino acids long. The putative signal sequence extends from amino acid positions 1 to 14. A putative cAMP- and cGMP-dependent protein kinase phosphorylation site is located at amino acid positions 33-36. Putative N-myristoylation sites are located at amino acid positions 50-55 and 87-92.

Clones DNA85066 and DNA94618 (designated as DNA85066-P2534 and DNA94618-P2534) have been deposited with ATCC and were assigned ATCC deposit nos. _____. The full-length hIL-1Ra1 protein shown in Figure 3 has an estimated molecular weight of about 21,822 daltons and a pI of about 8.9.

Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence, hIL-1Ra1 shows significant amino acid sequence identity to hIL-1Ra and hIL-1Ra β proteins.

The entire nucleotide sequence of the clone W08205, designated DNA92505, is shown in Figure 9 (SEQ ID NO: ____). Clone DNA92505 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 145-147, and a stop codon at nucleotide positions 610-612 (Fig. 9; SEQ ID NO: ____). The predicted polypeptide precursor (mIL-1Ra3) is 155 amino acids long. The putative signal sequence extends from amino acid positions 1-33. Putative N-myristoylation sites are located at amino acid positions 29-34, 60-65, 63-68, 91-96 and 106-111. An interleukin-1-like sequence is located at amino acid positions 111-131.

Clone DNA92505 (designated as DNA92505-P2534) was deposited with ATCC and was assigned ATCC deposit no. _____. The full length mL-1Ra3 protein shown in Figure 9 has an estimated molecular weight of about 17,134 daltons and a pI of about 4.8.

Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence, mL-1Ra3 shows significant amino acid sequence identity to mL-1Ra, hIL-1Ra, hIL-1Ra and hIL-1Ra β proteins.

EXAMPLE 2

Isolation of DNA encoding hIL-1ra2 and hIL-1Ra3

A expressed sequence tag (EST) DNA database (LIFESEQ[®], Incyte Pharmaceuticals, Palo Alto, CA) was searched with human interleukin-1 receptor antagonist (hIL-1Ra) sequence, and the ESTs, designated 1433156 (Figure 5, SEQ ID NO: __) and 5120028 (Figure 7, SEQ ID NO:), were identified, which showed homology with the hIL-1Ra known protein.

EST clones 1433156 and 5120028 were purchased from Incyte Pharmaceuticals (Palo Alto, CA) and the cDNA inserts were obtained and sequenced in their entireties.

The entire nucleotide sequence of the clone 1433156, designated DNA92929, is shown in Figure 5 (SEQ ID NO:). Clone DNA92929 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 96-98, and a stop codon at nucleotide positions 498-500 (Fig. 5; SEQ ID NO:). The predicted polypeptide precursor (hIL-1Ra2) is 134 amino acids long. The putative signal sequence extends from amino acid positions 1-26.

Clone DNA92929 (designated as DNA92929-P2534) was deposited with ATCC and was assigned ATCC deposit no. _____. The full-length hIL-1ra2 protein shown in Figure 5 has an estimated molecular weight of about 14,927 daltons and a pI of about 4.8.

Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence, hIL-1Ra2 shows significant amino acid sequence identity to hIL-1Ra β protein. hIL-1Ra2 is believed to be a splice variant of hIL-1Ra β .

The entire nucleotide sequence of the clone 5120028, designated DNA96787, is shown in Figure 7 (SEQ ID NO:). Clone DNA96787 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 1-3, and a stop codon at nucleotide positions 466-468 (Fig. 7; SEQ ID NO:). The predicted polypeptide precursor (hIL-1Ra3) is 155 amino acids long. The putative signal sequence extends from amino acid positions 1-33. Putative N-myristoylation sites are located at amino acid positions 29-34, 60-65, 63-68, 73-78, 91-96 and 106-111. An interleukin-1-like sequence is located at amino acid positions 111-131.

Clone DNA96787 (designated as DNA96787-P2534) was deposited with ATCC and was assigned ATCC deposit no. _____. The full length hIL-1Ra3 protein shown in Figure 7 has an estimated molecular weight of about 16,961 daltons and a pI of about 4.9.

Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length

sequence, hIL-1Ra3 shows significant amino acid sequence identity to hIL-1Ra and hIL-1Ra proteins.

EXAMPLE 3

Northern Blot Analysis

Expression of hIL-1Ra3 mRNA in human tissues and mIL-1Ra3 mRNA in mouse tissues was examined by Northern blot analysis. Human and mouse multiple tissue northern (RNA) blots and mouse embryo blots were purchased from Clontech and probed with corresponding cDNA according to the manufacturer's instructions.

As shown in Fig. 11, hIL-1Ra3 mRNA (2.7 kb) were detected only in human placenta and mIL-1Ra3 mRNA transcripts (1.4 kb and 2.5 kb) were detected only in the day-17 mouse embryo.

EXAMPLE 4

Use of IL-1lp as a hybridization probe

The following method describes use of a nucleotide sequence encoding IL-1lp as a hybridization probe.

DNA comprising the coding sequence of full-length or mature IL-1lp (as shown in Figures 3, 5, 7 and 9, SEQ ID NOS: ____) is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of IL-1lp) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled IL-1lp-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence IL-1lp can then be identified using standard techniques known in the art.

EXAMPLE 5

Expression of IL-1lp in *E. coli*

This example illustrates preparation of an unglycosylated form of IL-1lp by recombinant expression in *E. coli*.

The DNA sequence encoding an IL-1lp is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar *et al.*, *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the IL-1lp coding region, lambda transcriptional

terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

5 Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized IL-11p protein
10 can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

EXAMPLE 6

Expression of IL-11p in mammalian cells

This example illustrates preparation of a potentially glycosylated form of IL-11p by recombinant expression in
15 mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the IL-11p DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the IL-11p DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-IL-11p.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to
20 confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-IL-11p DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for
25 about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml ³⁵S-cysteine and 200 µCi/ml ³⁵S-methionine. After a 12 hour incubation,
30 the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of IL-11p polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, IL-11p may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci. USA*, 12: 7575 (1981). 293 cells are grown to maximal density in
35 a spinner flask and 700 µg pRK5-IL-11p DNA is added. The cells are first concentrated from the spinner flask by

centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed IL-11p can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, IL-11p can be expressed in CHO cells. The pRK5-IL-11p can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of IL-11p polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed IL-11p can then be concentrated and purified by any selected method.

Epitope-tagged IL-11p may also be expressed in host CHO cells. The IL-11p may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged IL-11p insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged IL-11p can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

EXAMPLE 7

Expression of IL-11p in Yeast

The following method describes recombinant expression of IL-11p in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of IL-11p from the ADH2/GAPDH promoter. DNA encoding IL-11p and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of IL-11p. For secretion, DNA encoding IL-11p can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native IL-11p signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of IL-11p.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant IL-11p can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing IL-11p may further be purified using selected column chromatography resins.

EXAMPLE 8

Expression of IL-11p in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of IL-11p in Baculovirus-infected insect cells.

The sequence coding for IL-11p is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding IL-11p or the desired portion of the coding sequence of IL-11p (such as the sequence encoding the mature protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (PharMingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley *et al.*, *Baculovirus expression vectors: A Laboratory Manual*, Oxford: Oxford University Press (1994).

Expressed poly-his tagged IL-11p can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert *et al.*, *Nature*, 362: 175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged IL-11p are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) IL-11p can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

EXAMPLE 9

IL-18 Receptor and IL-1 Receptor Binding of hIL-1Ra1

To facilitate the characterization of hIL-1Ra1, a PCR fragment containing the partial ORF of clone DNA85066 (Figure 1; SEQ ID NO:) was cloned into pCMV1FLAG (IBI Kodak, described in Pan *et al.*, *Science* 276, 111-113) as an

in-frame fusion to a NH₂-terminal preprotrypsin leader sequence and FLAG tag encoded by the vector. The entire cDNA insert of the recombinant pCMV1FLAG vector clone (designated clone DNA96786) was sequenced (Figure 2; SEQ ID NO:). The cDNAs encoding the extracellular domain of hIL1R and hIL18R (formerly known as hIL1Rrp) were obtained by polymerase chain reaction (PCR) and cloned into a modified pCMV1FLAG vector that allowed for in-frame fusion with the Fe portion of human immunoglobulin G.

Human embryonic kidney 293 cells were grown in high glucose DMEM (Genentech, Inc). The cells were seeded at 3-4 X10⁶ per plate (100 mm) and co-transfected with pCMV1FLAG-IL-1Ra1 and pCMV1FLAG-IL1R-ECD-Fc or pCMV1FLAG-IL18R-ECD-Fc by means of calcium phosphate precipitation. The media were changed 12 hours post transfection. The resultant conditioned media (10 ml each) were harvested after a further 70-74 hour incubation, clarified by centrifugation, aliquoted and stored at -70°C. The receptor-Fc and ligand complex from 1.5 ml conditioned medium was immunoprecipitated with protein G-Sepharose, washed three times with buffer containing 50 mM Hepes, pH7.0, 150 mM NaCl, 1 mM EDTA, 1% NP-40, and a protease inhibitor cocktail (BMB) and resolved on a 10-20% SDS-PAGE gel. The bound ligand was identified by immunoblotting using anti-FLAG monoclonal antibody (BMB).

As shown in Figure 13, the secreted FLAGhIL-1Ra1 fusion protein bound to IL-18R ECD and did not bind to IL-1R ECD, which indicates that hIL-1Ra1 could be an agonist or antagonist of IL-18R.

EXAMPLE 10

IL-1 Receptor and IL-18 Receptor Binding of mIL-1Ra3

cDNA encoding mIL-1Ra3 (DNA92505 shown in Figure 9; SEQ ID NO:) was cloned into pRK7 with a carboxy-terminal FLAG-tag. The resulting expression construct was transfected into human embryonic kidney 293 cells by means of calcium phosphate precipitation. 84-90 post transfection, the conditioned media containing secreted FLAGmIL-1Ra3 fusion protein was harvested. Conditioned media containing secreted IL-18R-Fc and IL-1R-Fc proteins were prepared as described in Example 9 above, with the exception that the 293 cells were transfected with either pCMV1FLAG-IL1R-ECD-Fc or pCMV1FLAG-IL18R-ECD-Fc alone (without pCMV1FLAG-IL-1Ra1 cotransfection).

For in vitro binding assays, IL-1R-Fc or IL-18R-Fc from 0.5 ml of the conditioned medium was immobilized to protein G-agarose and then mixed with 1.2 ml conditioned medium containing FLAGmIL-1Ra3. The receptor-ligand complexes were washed and resolved on an 10-20% SDS-PAGE gel and the bound ligand was detected by immunoblotting using anti-FLAG monoclonal antibody (Boehringer Mannheim).

As shown in Figure 14, FLAGmIL-1Ra3 fusion protein bound to IL-1R ECD and did not bind to IL-18R ECD. Since the amino acid sequence of mIL-1Ra3 is related to that of the known interleukin-1 receptor antagonist protein (IL-1Ra), mIL-3Ra3 is believed to be a novel IL-1 receptor antagonist.

EXAMPLE 11

Preparation of Antibodies that Bind IL-1)p

This example illustrates preparation of monoclonal antibodies which can specifically bind IL-11p.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified IL-11p, fusion proteins containing IL-11p, and cells expressing recombinant IL-11p on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the IL-11p immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-IL-11p antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of IL-11p. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against IL-11p. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against IL-11p is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-IL-11p monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

* * * *

Deposit of Material

The following materials have been deposited with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC):

<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
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This deposit was made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposit will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC §122 and the Commissioner's rules pursuant thereto (including 37 CFR §1.14 with particular reference to 886 OG 638).

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The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

20

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

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What is claimed is:

1. An isolated DNA molecule selected from the group consisting of: (1) a DNA molecule encoding an hIL-1Ra1 polypeptide comprising the amino acid sequence of amino acid residues from about 37 to about 203 of Figure 2 (SEQ ID NO:); (2) a DNA molecule encoding an hIL-1Ra1 polypeptide comprising the amino acid sequence of amino acid residues from about 15 to about 193 of Figure 3 (SEQ ID NO:); (3) a DNA molecule encoding an hIL-1Ra2 polypeptide comprising the amino acid sequence of amino acid residues from about 1 to about 134 of Figure 5 (SEQ ID NO:); (4) a DNA molecule encoding an hIL-1Ra2 fusion variant polypeptide consisting of a native amino acid sequence of hIL-1Ra2 having amino acid residues from about 27 to about 134 of Figure 5 (SEQ ID NO:) fused at its N-terminus or C-terminus to a heterologous amino acid or amino acid sequence; (5) a DNA molecule encoding an hIL-1Ra2 polypeptide consisting of the amino acid sequence of amino acid residues from about 27 to about 134 of Figure 5 (SEQ ID NO:); (6) a DNA molecule encoding an hIL-1Ra3 polypeptide comprising the amino acid sequence of amino acid residues from about 95 to about 134 of Figure 7 (SEQ ID NO:); (7) a DNA molecule encoding a mL-1Ra3 polypeptide comprising the amino acid sequence of amino acid residues from about 95 to about 134 of Figure 9 (SEQ ID NO:); and (8) the complement of any of the DNA molecules of (1)-(7).

2. The isolated DNA molecule of Claim 1 selected from the group consisting of: (1) a DNA molecule encoding an hIL-1Ra1 polypeptide comprising the amino acid sequence of amino acid residues from about 16 to about 203 of Figure 2 (SEQ ID NO:); (2) a DNA molecule encoding an hIL-1Ra1 polypeptide comprising the amino acid sequence of amino acid residues from about 1 to about 193 of Figure 3 (SEQ ID NO:); (3) a DNA molecule encoding an hIL-1Ra3 polypeptide comprising the amino acid sequence of amino acid residues from about 34 to about 155 of Figure 7 (SEQ ID NO:); (4) a DNA molecule encoding a mL-1Ra3 polypeptide comprising the amino acid sequence of amino acid residues from about 34 to about 155 of Figure 9 (SEQ ID NO:); and (5) the complement of any of the DNA molecules of (1)-(4).

3. The isolated DNA molecule of Claim 2 selected from the group consisting of: (1) a DNA molecule encoding an hIL-1Ra3 polypeptide comprising the amino acid sequence of amino acid residues from about 1 to about 155 of Figure 7 (SEQ ID NO:); (2) a DNA molecule encoding a mL-1Ra3 polypeptide comprising the amino acid sequence of amino acid residues from about 1 to about 155 of Figure 9 (SEQ ID NO:); and (3) the complement of any of the DNA molecules of (1)-(2).

4. The isolated DNA molecule of Claim 1 selected from the group consisting of: (1) a DNA molecule which encodes an hIL-1Ra1 polypeptide, and which comprises the nucleic acid sequence of nucleotide positions from about 118 to about 618 in the sense strand of Figure 2 (SEQ ID NO:); (2) a DNA molecule which encodes an hIL-1Ra1 polypeptide, and which comprises the nucleic acid sequence of nucleotide positions from about 145 to about 681 in the sense strand of Figure 3 (SEQ ID NO:); (3) a DNA molecule which encodes an hIL-1Ra2 polypeptide, and which comprises the nucleic acid sequence of nucleotide positions from about 96 to about 497 in the sense strand of Figure 5 (SEQ ID NO:); (4) a DNA

molecule which encodes an hIL-1Ra2 fusion variant polypeptide consisting of a native amino acid sequence of hIL-1Ra2 having amino acid residues from about 27 to about 134 of Figure 5 (SEQ ID NO:) fused at its N-terminus or C-terminus to a heterologous amino acid or amino acid sequence, and which comprises the nucleic acid sequence in the sense strand of Figure 5 (SEQ ID NO:) that encodes the native amino acid sequence; (5) a DNA molecule which encodes an hIL-1Ra2 polypeptide consisting of a native amino acid sequence of hIL-1Ra2 having amino acid residues from about 27 to about 134 of Figure 5 (SEQ ID NO:), and which comprises the nucleic acid sequence in the sense strand of Figure 5 (SEQ ID NO:) that encodes the native amino acid sequence; (6) a DNA molecule which encodes an hIL-1Ra3 polypeptide, and which comprises the nucleic acid sequence of nucleotide positions from about 283 to about 402 in the sense strand of Figure 7 (SEQ ID NO:); (7) a DNA molecule which encodes a mL-1Ra3 polypeptide, and which comprises the nucleic acid sequence of nucleotide positions from about 427 to about 546 in the sense strand of Figure 9 (SEQ ID NO:); and (8) the complement of any of the DNA molecules of (1)-(7).

5. The isolated nucleic acid molecule of Claim 4 selected from the group consisting of: (1) a DNA molecule comprising the nucleic acid sequence of nucleotide positions from about 103 to about 681 in the sense strand of Figure 3 (SEQ ID NO:); (2) a DNA molecule comprising the nucleic acid sequence of nucleotide positions from about 100 to about 465 in the sense strand of Figure 7 (SEQ ID NO:); (3) a DNA molecule comprising the nucleic acid sequence of nucleotide positions from about 244 to about 609 in the sense strand of Figure 9 (SEQ ID NO:); and (4) the complement of any of the DNA molecules of (1)-(3).

6. The isolated nucleic acid molecule of Claim 4 comprising (a) the complete DNA sequence in the sense strand of Figure 2 (SEQ ID NO:), Figure 3 (SEQ ID NO:), Figure 5 (SEQ ID NO:), Figure 7 (SEQ ID NO:), or Figure 9 (SEQ ID NO:), or the complement of (a).

7. An isolated nucleic acid molecule encoding an IL-1p polypeptide, comprising DNA hybridizing to the complement of a nucleic acid sequence selected from the group consisting of: (1) the nucleic acid sequence consisting of nucleotide positions from about 145 to about 180 in the sense strand of Figure 3 (SEQ ID NO:); (2) the nucleic acid sequence consisting of nucleotide positions from about 238 to about 465 in the sense strand of Figure 7 (SEQ ID NO:); and (3) the nucleic acid sequence consisting of nucleotide positions from about 424 to about 609 in the sense strand of Figure 9 (SEQ ID NO:).

8. An isolated nucleic acid molecule comprising (a) a DNA molecule encoding a polypeptide selected from the group consisting of: (1) a polypeptide comprising the mature hIL-1Ra1 polypeptide encoded by the cDNA insert in the vector deposited as ATCC Deposit No. (DNA85066-P2534); (2) a polypeptide comprising the mature hIL-1Ra1 polypeptide encoded by the cDNA insert in the vector deposited as ATCC Deposit No. (DNA96786-P2534); (3) a polypeptide consisting of the mature hIL-1Ra2 polypeptide encoded by the cDNA insert in the vector deposited as ATCC Deposit No.

(DNA92929-P2534), which mature hIL-1Ra2 polypeptide is fused at its N-terminus or C-terminus to a heterologous amino acid or amino acid sequence; (4) a polypeptide consisting of the mature hIL-1Ra2 polypeptide encoded by the cDNA insert in the vector deposited as ATCC Deposit No. (DNA92929-P2534); (5) a polypeptide comprising the mature hIL-1Ra3 polypeptide encoded by the cDNA insert in the vector deposited as ATCC Deposit No. (DNA96787-P2534); and (6) a polypeptide comprising the mature mIL-1Ra3 polypeptide encoded by the cDNA insert in the vector deposited as ATCC Deposit No. (DNA92505-P2534); or (b) the complement of the DNA molecule of (a).

9. An isolated nucleic acid molecule comprising (a) DNA encoding the IL-11p polypeptide of Claim 19, or (b) the complement of the DNA of (a).

10. An isolated nucleic acid molecule comprising (a) DNA encoding the IL-11p polypeptide of Claim 21, or (b) the complement of the DNA of (a).

11. A vector comprising the nucleic acid of Claim 1.

12. The vector of Claim 11 operably linked to control sequences recognized by a host cell transfected with the vector.

13. A host cell comprising the vector of Claim 11.

14. The host cell of Claim 13, wherein said cell is a CHO cell.

15. The host cell of Claim 13, wherein said cell is an *E. coli* cell.

16. The host cell of Claim 13, wherein said cell is a yeast cell.

17. A process for producing the IL-11p polypeptide of Claim 19 comprising the steps of: (1) culturing a host cell comprising a vector comprising a nucleic acid sequence that encodes the IL-11p polypeptide under conditions suitable for expression of said IL-11p polypeptide; and (2) recovering said IL-11p polypeptide from the cell culture.

18. An isolated IL-11p polypeptide encoded by the nucleic acid molecule of Claim 1.

19. An isolated IL-11p polypeptide selected from the group consisting of: (1) an hIL-1Ra1 polypeptide consisting of an amino acid sequence having at least an 80% sequence identity to the sequence of amino acid residues from about 37 to about 63 of Figure 2 (SEQ ID NO:); (2) an hIL-1Ra1 polypeptide consisting of an amino acid sequence having at least an 80% sequence identity to the sequence of amino acid residues from about 15 to about 53 of Figure 3 (SEQ ID NO:); (3)

- an hLL-1Ra2 polypeptide comprising the amino acid sequence of amino acid residues from about 1 to about 134 of Figure 5 (SEQ ID NO:); (4) an hLL-1Ra2 polypeptide consisting of the amino acid sequence of amino acid residues from about 27 to about 134 of Figure 5 (SEQ ID NO:); (5) an hLL-1Ra2 fusion variant polypeptide consisting of a native amino acid sequence of hLL-1Ra2 having amino acid residues from about 27 to about 134 of Figure 5 (SEQ ID NO:) fused at its N-terminus or C-terminus to a heterologous amino acid or amino acid sequence; (6) an hLL-1Ra3 polypeptide consisting of an amino acid sequence having at least an 80% sequence identity to the sequence of amino acid residues from about 95 to about 134 of Figure 7 (SEQ ID NO:); and (7) a mL-1Ra3 polypeptide consisting of an amino acid sequence having at least an 80% sequence identity to the sequence of amino acid residues from about 95 to about 134 of Figure 9 (SEQ ID NO:).
20. The isolated polypeptide of Claim 19 that is an hLL-1Ra3 polypeptide consisting of an amino acid sequence having at least an 80% sequence identity to the sequence of amino acid residues from about 80 to about 155 of Figure 7 (SEQ ID NO:).
21. The isolated polypeptide of Claim 19 selected from the group consisting of: (1) an hLL-1Ra1 polypeptide comprising amino acid residues from about 37 to about 63 of Figure 2 (SEQ ID NO:); (2) an hLL-1Ra1 polypeptide comprising amino acid residues from about 15 to about 53 of Figure 3 (SEQ ID NO:); (3) an hLL-1Ra2 polypeptide comprising amino acid residues from about 1 to about 134 of Figure 5 (SEQ ID NO:); (4) an hLL-1Ra2 polypeptide comprising amino acid residues from about 27 to about 134 of Figure 5 (SEQ ID NO:); (5) an hLL-1Ra2 fusion variant polypeptide consisting of a native amino acid sequence of hLL-1Ra2 having amino acid residues from about 27 to about 134 of Figure 5 (SEQ ID NO:) fused at its N-terminus or C-terminus to a heterologous amino acid or amino acid sequence; (6) an hLL-1Ra3 polypeptide comprising amino acid residues from about 95 to about 134 of Figure 7 (SEQ ID NO:); and (7) a mL-1Ra3 polypeptide comprising amino acid residues from about 95 to about 134 of Figure 9 (SEQ ID NO:).
22. The isolated polypeptide of Claim 21 selected from the group consisting of: (1) an hLL-1Ra1 polypeptide comprising amino acid residues from about 37 to about 203 of Figure 2 (SEQ ID NO:); (2) an hLL-1Ra1 polypeptide comprising amino acid residues from about 15 to about 193 of Figure 3 (SEQ ID NO:); (3) an hLL-1Ra3 polypeptide comprising amino acid residues from about 34 to about 155 of Figure 7 (SEQ ID NO:); and (3) a mL-1Ra3 polypeptide comprising amino acid residues from about 34 to about 155 of Figure 9 (SEQ ID NO:).
23. An isolated IL-1p polypeptide consisting of an amino acid sequence scoring at least 80% positives when compared to an amino sequence selected from the group consisting of: (1) amino acid residues from about 37 to about 63 of Figure 2 (SEQ ID NO:); (2) amino acid residues from about 15 to about 53 of Figure 3 (SEQ ID NO:); (3) amino acid residues from about 95 to about 134 of Figure 7 (SEQ ID NO:); and (4) amino acid residues from about 95 to about 134 of Figure 9 (SEQ ID NO:).

24. The isolated polypeptide of Claim 23 that is an hIL-1Ra3 polypeptide consisting of an amino acid sequence scoring at least 80% positives when compared to the sequence of amino acid residues from about 80 to about 155 of Figure 7.

25. An isolated IL-1lp polypeptide comprising an amino acid sequence sufficient to provide an anti-IL-1lp antibody binding site, which amino acid sequence coincides with any stretch of at least about 10 contiguous amino acids in a sequence selected from the group consisting of: (1) amino acid residues from about 37 to about 63 of Figure 2 (SEQ ID NO:); (2) amino acid residues from about 15 to about 53 of Figure 3 (SEQ ID NO:); (3) amino acid residues from about 80 to about 155 of Figure 7 (SEQ ID NO:); and (4) amino acid residues from about 95 to about 155 of Figure 9 (SEQ ID NO:).

26. An isolated IL-1lp polypeptide that is the same as the mature polypeptide encoded by the cDNA insert of a vector selected from the group consisting of the vectors deposited as ATCC Deposit Nos. (DNA85066-P2534), (DNA96786-P2534), (DNA92929-P2534), (DNA96787-P2534), and (DNA92505-P2534).

27. The IL-1lp polypeptide of Claim 21 that comprises a native amino acid sequence of the IL-1lp fused at its C-terminus or N-terminus to a heterologous amino acid sequence.

28. The IL-1lp polypeptide of Claim 27, wherein said heterologous amino acid sequence is an epitope tag sequence.

29. The IL-1lp polypeptide of Claim 27, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

30. An antibody which specifically binds to the IL-1lp polypeptide of claim 19.

31. The antibody of Claim 30, wherein said antibody is a monoclonal antibody.

Abstract of the Disclosure

The present invention is directed to novel polypeptides having homology to the IL-1-like family of proteins and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to
5 heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention, and methods for producing the polypeptides of the present invention.